

3040

RAW SEQUENCE LISTING

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Application Serial Number: 10/S22,096
Source: PCT
Date Processed by STIC: 2-2-05

ENTERED



PCT

RAW SEQUENCE LISTING

DATE: 02/02/2005

PATENT APPLICATION: US/10/522,096

TIME: 15:35:07

Input Set : A:\Sequence listing.txt

Output Set: N:\CRF4\02022005\J522096.raw

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3 <110> APPLICANT: Ehrhardt, Thomas
4   Sonnewald, Uwe
5   Bornke, Frederik
6   Chen, Shuai
8 <120> TITLE OF INVENTION: Sucrose-6-Phosphate Phosphatase as Target for Herbicides
10 <130> FILE REFERENCE: 532622010200
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/522,096
13 <141> CURRENT FILING DATE: 2005-01-24
15 <160> NUMBER OF SEQ ID NOS: 19
17 <170> SOFTWARE: PatentIn version 3.1
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 1278
21 <212> TYPE: DNA
22 <213> ORGANISM: Nicotiana tabacum
24 <220> FEATURE:
25 <221> NAME/KEY: CDS
26 <222> LOCATION: (1)..(1275)
27 <223> OTHER INFORMATION:
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35 gac cat aca atg gta gat cat cat gat gcc gag aac ctt tct ctg ctt      96
36 Asp His Thr Met Val Asp His His Asp Ala Glu Asn Leu Ser Leu Leu
37          20          25          30
39 aga ttt aat gct tta tgg gag gcg aat tat cgt gat aac tct ttg tta      144
40 Arg Phe Asn Ala Leu Trp Glu Ala Asn Tyr Arg Asp Asn Ser Leu Leu
41          35          40          45
43 gtg ttc tca act ggg aga tca cct aca ctt tac aag gag ttg agg aaa      192
44 Val Phe Ser Thr Gly Arg Ser Pro Thr Leu Tyr Lys Glu Leu Arg Lys
45          50          55          60
47 gaa aag ccc atg cta acc cca gat att act att atg tcg gtg gga act      240
48 Glu Lys Pro Met Leu Thr Pro Asp Ile Thr Ile Met Ser Val Gly Thr
49 65          70          75          80
51 gaa ata aca tat ggt aac tct gtg gtg cct gat gat ggt tgg gaa gct      288
52 Glu Ile Thr Tyr Gly Asn Ser Val Val Pro Asp Asp Gly Trp Glu Ala
53          85          90          95
55 ttt cta aat aac aag tgg gac aga aag ata gta aca gag gag act agc      336
56 Phe Leu Asn Asn Lys Trp Asp Arg Lys Ile Val Thr Glu Glu Thr Ser
57          100          105          110
59 aag ttt cct gaa ctc act cta cag tca gaa acg gag cag cga cca cac      384
60 Lys Phe Pro Glu Leu Thr Leu Gln Ser Glu Thr Glu Gln Arg Pro His
61          115          120          125

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63	aag gtc agt ttc tat gtt cag aaa gac aaa gca caa gat ata atg aaa	432
64	Lys Val Ser Phe Tyr Val Gln Lys Asp Lys Ala Gln Asp Ile Met Lys	
65	130 135 140	
67	act ctt tcc aag cgc ttc gaa gaa cgt ggg ctg gat gtc aaa ata att	480
68	Thr Leu Ser Lys Arg Phe Glu Glu Arg Gly Leu Asp Val Lys Ile Ile	
69	145 150 155 160	
71	tac agt gga ggc atg gat cta gat ata tta cca caa ggt gct ggc aaa	528
72	Tyr Ser Gly Gly Met Asp Leu Asp Ile Leu Pro Gln Gly Ala Gly Lys	
73	165 170 175	
75	gga caa gca ctt gca tat ttg ctt aag aaa ttg aag agt gag gga aaa	576
76	Gly Gln Ala Leu Ala Tyr Leu Leu Lys Lys Leu Lys Ser Glu Gly Lys	
77	180 185 190	
79	tta cca aac aac acc ctt gcc tgt ggt gac tct ggg aat gat gct gag	624
80	Leu Pro Asn Asn Thr Leu Ala Cys Gly Asp Ser Gly Asn Asp Ala Glu	
81	195 200 205	
83	cta ttc agt atc cca gat gtg tat ggt gta atg gta gct aat gca cag	672
84	Leu Phe Ser Ile Pro Asp Val Tyr Gly Val Met Val Ala Asn Ala Gln	
85	210 215 220	
87	gag gaa tta ttg caa tgg cat gct gca aat gcg aag aat aat cct aaa	720
88	Glu Glu Leu Leu Gln Trp His Ala Ala Asn Ala Lys Asn Asn Pro Lys	
89	225 230 235 240	
91	gta att cat gca aca gag agg tgt gct gcc ggt atc ata caa gct att	768
92	Val Ile His Ala Thr Glu Arg Cys Ala Ala Gly Ile Ile Gln Ala Ile	
93	245 250 255	
95	ggt cat tcc aac cta ggt cca agt acc tcc cct aga gat gtt atg gat	816
96	Gly His Ser Asn Leu Gly Pro Ser Thr Ser Pro Arg Asp Val Met Asp	
97	260 265 270	
99	ttg tca gac tgc aag atg gag aac ttt gtt ccc gcc tat gaa gtt gtc	864
100	Leu Ser Asp Cys Lys Met Glu Asn Phe Val Pro Ala Tyr Glu Val Val	
101	275 280 285	
103	aaa ttt tac cta ttt ttt gag aaa tgg agg cgt gga gaa att gag cat	912
104	Lys Phe Tyr Leu Phe Phe Glu Lys Trp Arg Arg Gly Glu Ile Glu His	
105	290 295 300	
107	tct gag cat tac ctg tca aac ctt aaa gca gtg tgt aga cca tct ggt	960
108	Ser Glu His Tyr Leu Ser Asn Leu Lys Ala Val Cys Arg Pro Ser Gly	
109	305 310 315 320	
111	act ttt gtc cac cca tct ggt gtt gag aaa tcc ctc cag gaa tgt gta	1008
112	Thr Phe Val His Pro Ser Gly Val Glu Lys Ser Leu Gln Glu Cys Val	
113	325 330 335	
115	act tta ttc ggg aca tgt cat ggt gac aaa cag ggg aaa caa ttt cgt	1056
116	Thr Leu Phe Gly Thr Cys His Gly Asp Lys Gln Gly Lys Gln Phe Arg	
117	340 345 350	
119	att tgg gtc gat caa gtt tta cct gta cag gtt ggt tcg gac tca tgg	1104
120	Ile Trp Val Asp Gln Val Leu Pro Val Gln Val Gly Ser Asp Ser Trp	
121	355 360 365	
123	tta gtg agt ttc aag aaa tgg gag ctc tct ggt gaa gac agg cga tgt	1152
124	Leu Val Ser Phe Lys Lys Trp Glu Leu Ser Gly Glu Asp Arg Arg Cys	
125	370 375 380	
127	tgc ata act aca gtc cta tta agt tca aag aat aag act gtc gca gat	1200

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128 Cys Ile Thr Thr Val Leu Leu Ser Ser Lys Asn Lys Thr Val Ala Asp
129 385          390          395          400
131 gga ctc act tgg acc cac gta cat cag aca tgg ctg aat gga gct gca      1248
132 Gly Leu Thr Trp Thr His Val His Gln Thr Trp Leu Asn Gly Ala Ala
133          405          410          415
135 gca agt gac tcc gcg tcc tgg ttc ttt tag      1278
136 Ala Ser Asp Ser Ala Ser Trp Phe Phe
137          420          425
140 <210> SEQ ID NO: 2
141 <211> LENGTH: 425
142 <212> TYPE: PRT
143 <213> ORGANISM: Nicotiana tabacum
145 <400> SEQUENCE: 2
147 Met Asp Gln Leu Thr Ser Ala Ala Arg Leu Met Ile Val Ser Asp Leu
148 1          5          10          15
151 Asp His Thr Met Val Asp His His Asp Ala Glu Asn Leu Ser Leu Leu
152          20          25          30
155 Arg Phe Asn Ala Leu Trp Glu Ala Asn Tyr Arg Asp Asn Ser Leu Leu
156          35          40          45
159 Val Phe Ser Thr Gly Arg Ser Pro Thr Leu Tyr Lys Glu Leu Arg Lys
160          50          55          60
163 Glu Lys Pro Met Leu Thr Pro Asp Ile Thr Ile Met Ser Val Gly Thr
164 65          70          75          80
167 Glu Ile Thr Tyr Gly Asn Ser Val Val Pro Asp Asp Gly Trp Glu Ala
168          85          90          95
171 Phe Leu Asn Asn Lys Trp Asp Arg Lys Ile Val Thr Glu Glu Thr Ser
172          100          105          110
175 Lys Phe Pro Glu Leu Thr Leu Gln Ser Glu Thr Glu Gln Arg Pro His
176          115          120          125
179 Lys Val Ser Phe Tyr Val Gln Lys Asp Lys Ala Gln Asp Ile Met Lys
180          130          135          140
183 Thr Leu Ser Lys Arg Phe Glu Glu Arg Gly Leu Asp Val Lys Ile Ile
184 145          150          155          160
187 Tyr Ser Gly Gly Met Asp Leu Asp Ile Leu Pro Gln Gly Ala Gly Lys
188          165          170          175
191 Gly Gln Ala Leu Ala Tyr Leu Leu Lys Lys Leu Lys Ser Glu Gly Lys
192          180          185          190
195 Leu Pro Asn Asn Thr Leu Ala Cys Gly Asp Ser Gly Asn Asp Ala Glu
196          195          200          205
199 Leu Phe Ser Ile Pro Asp Val Tyr Gly Val Met Val Ala Asn Ala Gln
200          210          215          220
203 Glu Glu Leu Leu Gln Trp His Ala Ala Asn Ala Lys Asn Asn Pro Lys
204 225          230          235          240
207 Val Ile His Ala Thr Glu Arg Cys Ala Ala Gly Ile Ile Gln Ala Ile
208          245          250          255
211 Gly His Ser Asn Leu Gly Pro Ser Thr Ser Pro Arg Asp Val Met Asp
212          260          265          270
215 Leu Ser Asp Cys Lys Met Glu Asn Phe Val Pro Ala Tyr Glu Val Val
216          275          280          285

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Input Set : A:\Sequence listing.txt

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219 Lys Phe Tyr Leu Phe Phe Glu Lys Trp Arg Arg Gly Glu Ile Glu His
220      290      295      300
223 Ser Glu His Tyr Leu Ser Asn Leu Lys Ala Val Cys Arg Pro Ser Gly
224 305      310      315      320
227 Thr Phe Val His Pro Ser Gly Val Glu Lys Ser Leu Gln Glu Cys Val
228      325      330      335
231 Thr Leu Phe Gly Thr Cys His Gly Asp Lys Gln Gly Lys Gln Phe Arg
232      340      345      350
235 Ile Trp Val Asp Gln Val Leu Pro Val Gln Val Gly Ser Asp Ser Trp
236      355      360      365
239 Leu Val Ser Phe Lys Lys Trp Glu Leu Ser Gly Glu Asp Arg Arg Cys
240      370      375      380
243 Cys Ile Thr Thr Val Leu Ser Ser Lys Asn Lys Thr Val Ala Asp
244 385      390      395      400
247 Gly Leu Thr Trp Thr His Val His Gln Thr Trp Leu Asn Gly Ala Ala
248      405      410      415
251 Ala Ser Asp Ser Ala Ser Trp Phe Phe
252      420      425

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255 <210> SEQ ID NO: 3

256 <211> LENGTH: 1278

257 <212> TYPE: DNA

258 <213> ORGANISM: Nicotiana tabacum

260 <220> FEATURE:

261 <221> NAME/KEY: CDS

262 <222> LOCATION: (1)..(1275)

263 <223> OTHER INFORMATION:

W--> 266 <400> 3

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267 atg gat cag cta acc agt gcc gca cgt ctc atg ata gtc tca gat ctt      48
268 Met Asp Gln Leu Thr Ser Ala Ala Arg Leu Met Ile Val Ser Asp Leu
269 1      5      10      15
271 gac cat acc atg gtt gat cat cat gat cct gag aac ctt tct ctg ctt      96
272 Asp His Thr Met Val Asp His His Asp Pro Glu Asn Leu Ser Leu Leu
273      20      25      30
275 agg ttt aat gct tta tgg gag gcc aat tat cgt gaa aac tcc ttg tta      144
276 Arg Phe Asn Ala Leu Trp Glu Ala Asn Tyr Arg Glu Asn Ser Leu Leu
277      35      40      45
279 gtg ttc tca act ggg aga tca cct acc ctt tac aag gag ttg aga aaa      192
280 Val Phe Ser Thr Gly Arg Ser Pro Thr Leu Tyr Lys Glu Leu Arg Lys
281      50      55      60
283 gag aag ccc atg cta acc cca gat att acc att atg tct gtg ggg act      240
284 Glu Lys Pro Met Leu Thr Pro Asp Ile Thr Ile Met Ser Val Gly Thr
285 65      70      75      80
287 gaa ata act tat ggt aac tct atg gag cca gat gat ggt tgg gaa gca      288
288 Glu Ile Thr Tyr Gly Asn Ser Met Glu Pro Asp Asp Gly Trp Glu Ala
289      85      90      95
291 ttt tta aat gat aag tgg gat cgg aaa ata gtg aca gag gag aca agc      336
292 Phe Leu Asn Asp Lys Trp Asp Arg Lys Ile Val Thr Glu Glu Thr Ser
293      100      105      110
295 aaa ttt cct gaa ctc acc ctt cag tca gaa aca gag cag cga cca cac      384

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Input Set : A:\Sequence listing.txt

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296 Lys Phe Pro Glu Leu Thr Leu Gln Ser Glu Thr Glu Gln Arg Pro His
297          115          120          125
299 aag gtc agt ttc tat gtt cag aaa gac aag gct caa gat ata acg gga      432
300 Lys Val Ser Phe Tyr Val Gln Lys Asp Lys Ala Gln Asp Ile Thr Gly
301          130          135          140
303 act ctt tcc aag cgc ttg gaa gaa cgt ggg ttg gat gtc aaa ata att      480
304 Thr Leu Ser Lys Arg Leu Glu Glu Arg Gly Leu Asp Val Lys Ile Ile
305 145          150          155          160
307 tat agc gga ggg atg gat ttg gac att ttg cca caa ggt gct ggc aaa      528
308 Tyr Ser Gly Gly Met Asp Leu Asp Ile Leu Pro Gln Gly Ala Gly Lys
309          165          170          175
311 gga cga gca ctt gca tat ttg ctt aag aaa tta aag agt gag ggc aag      576
312 Gly Arg Ala Leu Ala Tyr Leu Leu Lys Lys Leu Lys Ser Glu Gly Lys
313          180          185          190
315 tta cca aac aac acg ctt gcc tgt ggt gac tct gga aat gat gct gag      624
316 Leu Pro Asn Asn Thr Leu Ala Cys Gly Asp Ser Gly Asn Asp Ala Glu
317          195          200          205
319 ctt ttc agt atc cca gat gtt tat ggt gtg atg gta gcg aat gca cag      672
320 Leu Phe Ser Ile Pro Asp Val Tyr Gly Val Met Val Ala Asn Ala Gln
321          210          215          220
323 gag gag tta tta caa tgg cgt gct gca aat gca aaa gat agt cca aaa      720
324 Glu Glu Leu Leu Gln Trp Arg Ala Ala Asn Ala Lys Asp Ser Pro Lys
325 225          230          235          240
327 gta att cat gca aca gag aga tgt gcc gcg ggt ata ata caa gca att      768
328 Val Ile His Ala Thr Glu Arg Cys Ala Ala Gly Ile Ile Gln Ala Ile
329          245          250          255
331 ggg cat ttc aac ctg gga cca aat acc tct cct aga gat gtt aca gat      816
332 Gly His Phe Asn Leu Gly Pro Asn Thr Ser Pro Arg Asp Val Thr Asp
333          260          265          270
335 atg tca gac tgc aag atg gag aat ttt gtt cct gct tat gaa gtc gtc      864
336 Met Ser Asp Cys Lys Met Glu Asn Phe Val Pro Ala Tyr Glu Val Val
337          275          280          285
339 aaa ttt tac ttg ttt ttc gag aaa tgg agg cgt gga gaa att gag aat      912
340 Lys Phe Tyr Leu Phe Phe Glu Lys Trp Arg Arg Gly Glu Ile Glu Asn
341          290          295          300
343 tct gac ctt cac ttg tca aac ctg aaa gca gtt tgt aga cca tcc ggt      960
344 Ser Asp Leu His Leu Ser Asn Leu Lys Ala Val Cys Arg Pro Ser Gly
345 305          310          315          320
347 act ttt gtg cac cca tct gga gtt gag aaa tat ctt gag gac tgc ata      1008
348 Thr Phe Val His Pro Ser Gly Val Glu Lys Tyr Leu Glu Asp Cys Ile
349          325          330          335
351 aat aca ttg aga act tgt cac ggt gac aaa cag ggt aaa caa ttt cgt      1056
352 Asn Thr Leu Arg Thr Cys His Gly Asp Lys Gln Gly Lys Gln Phe Arg
353          340          345          350
355 att tgg gtt gat cta gtg tta cct aca cag gtt ggt tca gat tca tgg      1104
356 Ile Trp Val Asp Leu Val Leu Pro Thr Gln Val Gly Ser Asp Ser Trp
357          355          360          365
359 tta gtg agt ttc aag aaa tgg gag ctt tgt ggc gaa gag cga caa tgt      1152
360 Leu Val Ser Phe Lys Lys Trp Glu Leu Cys Gly Glu Glu Arg Gln Cys

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VERIFICATION SUMMARY

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PATENT APPLICATION: US/10/522,096

TIME: 15:35:08

Input Set : A:\Sequence listing.txt

Output Set: N:\CRF4\02022005\J522096.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application Number
L:30 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:27
L:266 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:263
L:502 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:499